

IN THE SPECIFICATION

At page 10, lines 16-19, please replace the fourth full paragraph with the following text:

Figs. 3A-3D depict a comparison of the amino acid sequences of GLUTX (SEQ ID NO:2), GLUT1 (SEQ ID NO:3), GLUT2 (SEQ ID NO:4), GLUT3 (SEQ ID NO:5), GLUT4 (SEQ ID NO:6), and GLUT5 (SEQ ID NO:7). A majority sequence is depicted to indicate conserved residues (SEQ ID NO:10).

At page 82, lines 13-27, please replace the paragraph with the following text:

The predicted amino acid sequence of GLUTX was compared to the amino acid sequences of GLUT1, (SEQ ID NO:3), GLUT2 (SEQ ID NO:4), GLUT3 (SEQ ID NO:5), GLUT4 (SEQ ID NO:6), and GLUT5 (SEQ ID NO:7). This comparison is depicted in Fig. 3 along with a majority sequence (SEQ ID NO:8 10). As noted above, in designing variant forms of GLUTX which retain the activity of wild-type GLUTX, it is generally preferable to avoid altering residues that are highly conserved. Of course, if one wished to design a reduced activity variant of GLUTX, it is generally preferable to alter conserved residues. Using sequence comparison information one can design GLUTX variants which are more similar to GLUT1, (SEQ ID NO:3), GLUT2 (SEQ ID NO:4), GLUT3 (SEQ ID NO:5), GLUT4 (SEQ ID NO:6), or GLUT5 (SEQ ID NO:7).